

Amendments to the Specification

Please replace the paragraph at page 14, line 27, through page 15, line 16, with the following amended paragraph:

As described herein, the *ospC* families of the present invention share about 98% homology at the nucleic acid level between strains of the same family and share no more than about 92% homology at the nucleic acid level between strains of different families. Determination of homology excludes any non-*ospC* sequences. Members of the same *ospC* family have similar antigenic profiles, e.g. elicit immune response against similar strains of Lyme disease causing *Borrelia*. The chimeric proteins of the present invention unexpectedly elicit immune response to Lyme disease causing *Borrelia* of different genospecies than the genospecies from which the component polypeptides were derived. In one embodiment of the present invention, *Borrelia burgdorferi* *ospC* family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, PKA, TXGW and strains of *Borrelia* containing *ospC* allele OC1. In another embodiment of the present invention, *Borrelia burgdorferi* *ospC* family B comprises strains 35B808, 61BV3, BUR, DK7, PB3, ZS7 and strains containing *ospC* alleles OC2 and OC3. In still another embodiment of the present invention, *Borrelia burgdorferi* *ospC* family I comprises strains 297, HB19 and strains containing *ospC* allele OC10, wherein strain 297 is characterized by *ospC* of GenBank Accession No. L42893 (SEQ ID NO:85). In still another embodiment of the present invention, *Borrelia burgdorferi* *ospC* family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* allele OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank Accession No. U08284 (SEQ ID NO:86).

Please replace the paragraph at page 30, lines 10 through 23 with the following amended paragraph:

Of the one hundred and thirty-two primary isolates from patients with Lyme disease in this study, most contained only a single strain. Seven skin isolates and one CSF isolate contained

two different strains as determined by SSCP analysis, thus giving a total of one hundred and forty different strains. The *ospC* allele pairs found in multiply infected erythema migrans biopsy specimens were (OC1, OC12), (OC1, OC14), 2x(OC2, OC3), 2x(OC2, OC12), and (OC8, OC18). CSF isolate NY940657 contained *ospC* alleles OC1 and OC12. For CSF isolate 297, which was isolated in Connecticut, there were two *ospC* sequences published in GenBank: L42893 (SEQ ID NO:85), which is analogous to OC10 and U08284 (SE ID NO:86), which is analogous to OC12. The pair-wise difference of *ospC* sequences of both strains is 16.4%, suggesting CNS infection with two different strains in this isolate. Overall, 5.5% of all isolates described herein contained two strains. Because as many as 50% of ticks isolated in the wild are infected with multiple strains, exposure to multiple strains in a single tick bite is common, raising the possibility that different strains are differentially pathogenic.